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RAW SEQUENCE LISTING

DATE: 01/03/2002

PATENT APPLICATION: US/09/902,853

TIME: 11:26:35

Input Set : N:\Crf3\RULE60\09902853.raw

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1 <110> APPLICANT: Genentech, Inc.
2 Ashkenazi, Avi
3 Botstein, David
4 Desnoyers, Luc
5 Eaton, Dan L.
6 Ferrara, Napoleone
7 Filvaroff, Ellen
8 Fong, Sherman
9 Gao, Wei-Qiang
10 Gerber, Hanspeter
11 Gerritsen, Mary E.
12 Goddard, A.
13 Godowski, Paul J.
14 Grimaldi, Christopher J.
15 Gurney, Austin L.
16 Hillan, Kenneth, J.
17 Kljavin, Ivar J.
18 Mather, Jennie P.
19 Pan, James
20 Paoni, Nicholas F.
21 Roy, Margaret Ann
22 Stewart, Timothy A.
23 Tumas, Daniel
24 Williams, P. Mickey
25 Wood, William, I.
26 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
27 Acids Encoding the Same
28 <130> FILE REFERENCE: 10466-14
29 <140> CURRENT APPLICATION NUMBER: 09/902,853
30 <141> CURRENT FILING DATE: 2001-07-10
31 <150> PRIOR APPLICATION NUMBER: US/09/665,350
32 <151> PRIOR FILING DATE: 2000-09-18
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37 <150> PRIOR APPLICATION NUMBER: US 60/146,222
38 <151> PRIOR FILING DATE: 1999-07-28
39 <150> PRIOR APPLICATION NUMBER: PCT/US99/20594
40 <151> PRIOR FILING DATE: 1999-09-08
41 <150> PRIOR APPLICATION NUMBER: PCT/US99/20944
42 <151> PRIOR FILING DATE: 1999-09-13
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45 <150> PRIOR APPLICATION NUMBER: PCT/US99/21547
46 <151> PRIOR FILING DATE: 1999-09-15
47 <150> PRIOR APPLICATION NUMBER: PCT/US99/23089

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74      tggagctccg gctgcgtctt cccgcagcgc taccgcctat gcgcctgccg 150
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82      gaagacaactg aaagtgtgct gctctccagg aacctacggt ccgcactgtc 550
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100     aaaattgacc attgtaggta atcaggagga aaaaaaaaaa aaaaaaaaaa 1450
101     aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500
102     gcccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca 1550
103     tcacaaatth cacaataaaa gcattttttt cactgcattc tagttgtggt 1600
104     ttgtccaaac tcatcaatgt atcttatcat gtctggatcg ggaattaatt 1650
105     cggcgagca ccatggcctg aaataacctc tgaaagagga acttggttag 1700
106     gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg tcagttaggg 1750
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118      20          25          30
119      Cys His Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met
120      35          40          45
121      Val Asp Thr Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp
122      50          55          60
123      Glu Glu Lys Thr Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu
124      65          70          75
125      Leu Glu Ile Leu Glu Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys
126      80          85          90
127      Asn Gln Met Leu Glu Ala Gln Glu Glu His Leu Glu Ala Trp Trp
128      95          100         105
129      Leu Gln Leu Lys Ser Glu Tyr Pro Asp Leu Phe Glu Trp Phe Cys
130      110         115         120
131      Val Lys Thr Leu Lys Val Cys Cys Ser Pro Gly Thr Tyr Gly Pro
132      125         130         135
133      Asp Cys Leu Ala Cys Gln Gly Gly Ser Gln Arg Pro Cys Ser Gly
134      140         145         150
135      Asn Gly His Cys Ser Gly Asp Gly Ser Arg Gln Gly Asp Gly Ser
136      155         160         165
137      Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu Cys Thr Asp Cys
138      170         175         180
139      Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr His Ser Ile
140      185         190         195
141      Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Leu Thr
142      200         205         210
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145      Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
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152		275		280		285
153	Gly Gln Cys Ala	Asp Val Asp Glu Cys	Ser Leu Ala Glu Lys Thr			
154		290		295		300
155	Cys Val Arg Lys	Asn Glu Asn Cys Tyr	Asn Thr Pro Gly Ser Tyr			
156		305		310		315
157	Val Cys Val Cys	Pro Asp Gly Phe Glu	Glu Thr Glu Asp Ala Cys			
158		320		325		330
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166 <212> TYPE: DNA
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171	cgcccagccg	tctaaacggg	aacagccctg	gctgagggag	ctgcagcgca	150
172	gcagagtatc	tgacggcgcc	aggttgcgta	ggtgcggcac	gaggagtttt	200
173	cccggcagcg	aggaggtcct	gagcagcatg	gcccggagga	gcgccttccc	250
174	tgccgccgcg	ctctggctct	ggagcatcct	cctgtgcctg	ctggcactgc	300
175	gggcgagggc	cgggccgcgc	caggaggaga	gcctgtacct	atggatcgat	350
176	gctcaccagg	caagagtact	cataggattt	gaagaagata	tcctgattgt	400
177	ttcagagggg	aaaatggcac	cttttacaca	tgatttcaga	aaagcgcaac	450
178	agagaatgcc	agctattcct	gtcaatatcc	attccatgaa	ttttacctgg	500
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180	cctggataaa	ggcatcatgg	cagatccaac	cgatcaatgtc	cctctgctgg	600
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182	ggaaaacagg	atgggggtgg	agcatttgaa	gtggatgtga	ttgttatgaa	700
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184	aaacatgtca	acaagctgag	tgcccaggcg	ggtgccgaaa	tggaggcttt	800
185	tgtaatgaaa	gacgcactcg	cgagtgtcct	gatgggttcc	acggacctca	850
186	ctgtgagaaa	gccctttgta	ccccacgatg	tatgaatggg	ggactttgtg	900
187	tgactcctgg	tttctgcata	tgcccacctg	gattctatgg	agtgaactgt	950
188	gacaaagcaa	actgctcaac	cacctgcttt	aatggaggga	cctgtttcta	1000
189	ccctggaaaa	tgtatttgcc	ctccaggact	agagggagag	cagtgtgaaa	1050
190	tcagcaaattg	cccacaaccc	tgtcgaaatg	gaggtaaattg	cattggtaaa	1100
191	agcaaattgta	agtgttccaa	aggttaccag	ggagacctct	gttcaaagcc	1150
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193	aatgccaatg	tcaagaaggt	tggcatggaa	gacactgcaa	taaaaggtac	1250
194	gaagccagcc	tcatacatgc	cctgaggcca	gcaggcgccc	agctcaggca	1300
195	gcacacgcct	tcacttaaaa	aggccgagga	gcggcgggat	ccacctgaat	1350
196	ccaattacat	ctggtgaact	ccgacatctg	aaacgtttta	agttacacca	1400
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201   tatgtcaatt gatcaggtta aaattttcag tgtgtagttg gcagatattt 1650
202   tcaaaattac aatgcattta tgggtgctgg gggcagggga acatcagaaa 1700
203   ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg atggtgcagt 1750
204   taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
205   ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata 1850
206   tattttgacc ttaccattat tccagagatt cagtattaaa aaaaaaaaaa 1900
207   ttacactgtg gtagtggcat ttaaacaata taatatattc taaacacaat 1950
208   gaaataggga atataatgta tgaacttttt gcattggcct gaagcaatat 2000
209   aatataattg aaacaaaaca cagctcttac ctaataaaca ttttatactg 2050
210   tttgtatgta taaaataaag gtgctgcttt agttttttgg aaaaaaaaaa 2100
211   aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgccgc gactctagag 2150
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223             20             25             30
224   Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala
225             35             40             45
226   Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu
227             50             55             60
228   Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln
229             65             70             75
230   Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr
231             80             85             90
232   Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser
233             95            100            105
234   Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn
235            110            115            120
236   Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln
237            125            130            135
238   Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe
239            140            145            150
240   Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu
241            155            160            165
242   Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala
243            170            175            180
244   Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg
245            185            190            195
246   Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu
247            200            205            210

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VERIFICATION SUMMARY

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